Interacting Monomer-Dimer Model with Infinitely Many Absorbing States

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We study a modified version of the interacting monomer-dimer (IMD) model that has infinitely many absorbing (IMA) states. Unlike all other previously studied models with IMA states, the absorbing states can be divided into two equivalent groups which are dynamically separated infinitely far apart. Monte Carlo simulations show that this model belongs to the directed Ising universality class like the ordinary IMD model with two equivalent absorbing states. This model is the first model with IMA states which does not belong to the directed percolation (DP) universality class. The DP universality class can be restored in two ways, i.e., by connecting the two equivalent groups dynamically or by introducing a symmetry-breaking field between the two groups.

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A wide variety of nonequilibrium systems with a single trapped (absorbing) state display a continuous phase transition from an active phase into an absorbing phase, which belongs to the directed percolation (DP) universality class [1–4]. Recently, systems with multiple absorbing states have been investigated extensively. The interacting monomer-dimer(IMD) model introduced by one of us [5] is one of many models that have two equivalent absorbing states [6–9]. These models belong to a different universality class from DP. By the analogy to the equilibrium Ising model that has two equivalent ground states, this new class is called as the directed Ising (DI) universality class [10]. When the (Ising) symmetry between the absorbing states is broken in the sense that one of the absorbing states is probabilistically preferable, the system goes back to the DP class [11]. Hence, the symmetry between the absorbing states is the key factor in determining the universality class of models with several absorbing states. Unfortunately, no models with higher symmetries than the Ising symmetry (like the three-state Potts symmetry) are found to have a stable absorbing phase as yet.

In contrast, systems with infinitely many absorbing (IMA) states are far less understood. All IMA systems studied so far belong to the DP universality class [12,13]. The number of absorbing states of these IMA systems grows exponentially with system size but there is no clear-cut symmetry among absorbing states. Recently, it was argued that the IMA models should belong to the DP class unless they possess any extra symmetry among absorbing states [14,15]. However, no IMA model with an additional symmetry has been studied up to date and the role of the symmetry in the IMA systems is still unclear.

In this Letter, we introduce an IMA model with the Ising symmetry between two groups of absorbing states. These two groups of absorbing states are equivalent and dynamically separated infinitely far apart. In other words, an absorbing state in one group can not be reached from any absorbing state in the other group by a finite number of successive local changes. There is no infinite dynamic barrier among absorbing states inside each group. This dynamic barrier is similar to the free energy barrier between ground states of equilibrium systems that exhibit spontaneous symmetry breaking in the ordered phase. Our numerical simulations show that this model belongs to the DI universality class. Furthermore, we find that this model crosses over to the DP class by allowing that the two absorbing groups are connected dynamically and/or by introducing a symmetry-breaking field to make one absorbing group probabilistically preferable to the other.

Our model is a modified version of the ordinary IMD model that we call the IMA-IMD model. Dynamic rules of the IMA-IMD model are almost the same as those of the IMD model with infinitely strong repulsion between the same species in one dimension [5]. A monomer (A) cannot adsorb at a nearest-neighbor site of an already-occupied monomer (restricted vacancy) but adsorbs at a free vacant site with no adjacent monomer-occupied sites. Similarly, a dimer (B_2) cannot adsorb at a pair of restricted vacancies (B in nearest-neighbor sites) but adsorbs at a pair of free vacancies. There are no nearest-neighbor restrictions in adsorbing particles of different species. Only the adsorption-limited reactions are considered. Adsorbed dimers dissociate and a nearest neighbor of the adsorbed A and B particles reacts, forms the AB product, and desorbs the catalytic surface immediately. Differentiation between the IMA-IMD model and the IMD model comes in when there is an A adsorption attempt at a vacant site between an adsorbed A and an adsorbed B. In the IMD model, we allow the A to adsorb and react with the neighboring B, so there are two equivalent absorbing states comprised of only monomers

at alternating sites, i.e., $(A0A0\cdots)$ and $(0A0A\cdots)$ where "0" represents a vacancy. In the IMA-IMD model, this process is disallowed. Then, any configuration can be an absorbing state if there are no nearest neighbor pair of vacancies and no single vacany between two B particles, e.g., $(\cdots B0A0BB0A0A\cdots)$. To impose the Ising symmetry between the absorbing states, we introduce the probability s of spontaneous desorption of a nearest neighbor pair of adsorbed B particles. At finite s, an absorbing configuration cannot have this BB pair. Hence only those configurations that have particles at alternating sites and no two B's at consecutive alternating sites become absorbing states, e.g., $(A0A0B0A0\cdots)$ and $(0A0A0B0A\cdots)$. The absorbing states are divided into two groups with particles occupied at odd- and even-numbered sites (O group and E group). The number of absorbing states in each group grows exponentially with system size and there is a one-to-one mapping between absorbing states in two groups. It is clear that one can not reach from an absorbing state in one group to an absorbing state in the other group by a finite number of successive local changes. Any interface (active region) between two absorbing states in the different groups never disappears by itself in a finite amount of time, so there is an infinite dynamic barrier between the two groups. These interfaces annihilate pairwise only.

The order parameter characterizing the absorbing phase transition is the density of active sites or kinks (domain walls). In the IMD model, the dimer density served well as the order parameter, but it cannot do in this model. We use the kink density as the order parameter. Kinks are defined such that all absorbing configurations have no kinks but any local change of the absorbing configurations should produce kinks. In this model, one should examine, at least, three adjacent sites to check the existence of kinks. There are 13 possible configurations for three adjacent sites. We assign a kink to eight different configurations; 000, 00A, A00, B00, 00B, $B0B$, $BB0$, and $0BB$. Five others, $A0A$, $A0B$, $B0A$, $0A0$, and $0B0$, do not have a kink. In this kink representation, there is no mod(2) conservation of the total number of kinks.

Three independent critical exponents characterize the critical behavior near the absorbing transition: the order parameter exponent β, correlation length exponent $\nu_\perp$, and relaxation time exponent $\nu_\parallel$ [2]. Elementary scaling theory combined with the finite size scaling theory [16] predicts that the kink density $\rho(p_c, L)$ at criticality in the (quasi)steady state scales with system size L as

$$\rho(p_c, L) \sim L^{-\beta/\nu_\perp}. \quad (1)$$

One can also expect the short time behavior of the kink density as $\rho(p_c, t) \sim t^{-\beta/\nu_\parallel}$ and the characteristic time scales with system size as $\tau(p_c, L) \sim L^{\nu_\parallel/\nu_\perp}$.

In Monte Carlo simulations, a monomer is attempted to adsorb at a randomly chosen site with probability $(1-s)p$ and a dimer with probability $(1-s)(1-p)$. With probability s, a randomly chosen nearest neighbor pair of adsorbed B's (if there is any) is desorbed from the lattice. We choose the dimer desorption probability $s = 0.5$ and run stationary Monte Carlo simulations starting with an empty lattice with size $L = 2^5$ up to 2^{11}. The system reaches a quasisteady state first and stays for a reasonably long time before finally entering into an absorbing state. We measure the kink density in the quasisteady state and average over many survived samples. The number of samples varies from 2×10^5 for $L = 2^5$ to 2×10^3 for $L = 2^{11}$. The number of time steps ranges from 10^3 to 2×10^5.

From Eq. (1), we expect the ratio of the critical kink densities for two successive system sizes $\rho(L/2)/\rho(L) = 2^{\beta/\nu_\perp}$, ignoring corrections to scaling. This ratio converges to unity in the active phase ($p < p_c$) and to 2 in the absorbing phase ($p > p_c$) in the limit $L \to \infty$. We plot the logarithm of this ratio divided by $\ln 2$ as a function of p for $L = 2^6, \cdots, 2^{11}$ in Fig. 1. The crossing points between lines for two successive sizes converge slowly due to strong corrections to scaling. In the limit $L \to \infty$, we estimate the crossing points converge to the point at $p_c = 0.425(4)$ and $\beta/\nu_\perp = 0.49(3)$. The value of $\beta/\nu_\perp$ agrees well with the standard DI value 0.50.

In Fig. 2, we show the time dependence of the critical kink densities $\rho(p_c, t)$ for various system sizes with $p_c = 0.425$. From the slope of $\rho(p_c, t)$ we estimate $\beta/\nu_\parallel = 0.275(5)$. Insets show the size dependence of the relaxation time $\tau(p_c, L)$ and the steady-state kink density $\rho(p_c, L)$ at criticality. We estimate $\nu_\parallel/\nu_\perp = 1.74(4)$ and $\beta/\nu_\perp = 0.494(6)$, respectively. All of these results are in excellent agreement with the DI values.

We run dynamic Monte Carlo simulations with various initial configurations and get a more precise estimate of the critical probability $p_c = 0.425(1)$. Our estimates for the dynamic scaling exponents are $\delta + \eta = 0.28(1)$ and $z = 1.14(1)$ [17], where $\delta + \eta$ characterizes the growth of the number of kinks averaged over survived samples and z the spreading of the active region [2]. These values are also in excellent agreement with the DI values.

To check the importance of the Ising symmetry among the absorbing states, we introduce a symmetry breaking field such that the monomer adsorption attempt at an even-numbered site is rejected with probability h [11]. For finite h, the O group of absorbing states is probabilistically preferable to the E group. We set $h = 0.1$ and run stationary Monte Carlo simulations for lattice sizes $L = 2^5$ up to 2^9. In Fig. 3, we plot $\ln[\rho(L/2)/\rho(L)]/\ln 2$ versus p, from which we estimate $p_c = 0.304(2)$ and $\beta/\nu_\perp = 0.24(1)$. The value of $\beta/\nu_\perp$ is clearly different from the DI value but agrees well with the standard DP value 0.2524(5). More detailed study including dynamic Monte Carlo simulations confirms that the systems with finite h belong to the DP universality class [17].

Similar to the case of the ordinary IMD model, the symmetry-breaking field makes the system behave like having only one (preferred) group of absorbing states [10]. Evolutions of the critical interfaces (active region) (a) for the symmetric case ($h = 0$) and (b) for the asymmetric case ($h = 0.1$) are shown in Fig. 4. In the symmetric case, the interfaces between the O and E group of absorbing states diffuse until they meet and form a loop to disappear, which is the essential characteristic of the DI universality class. In the asymmetric case, the absorbing region of the unpreferred (E) group quickly vanishes and the interfaces between the different groups become irrelvant. The interfaces inside the preferred (O) group, which can disappear by themselves without forming loops, become dominant and force the system into the DP universality class.

When the desorption process of a nearest neighbor BB pair is forbidden ($s = 0$), the system can find many more absorbing states with BB pairs, e.g., $(\cdots B0A0BB0A0A\cdots)$, in addition to the two groups of the absorbing states for $s \neq 0$. These new extra absorbing states are generically mixtures of the O and E group of the absorbing states. The O and E groups are now connected dynamically via new mixture-type absorbing states. Consider a configuration with an interface between two absorbing states in the different groups, $(\cdots B0A0\underline{000}A0A\cdots)$, where the interface is placed in two central vacancies $\underline{00}$. With nonzero s, this configuration never evolves into an absorbing state. However, in the case of $s = 0$, it can evolve into a mixture-type absorbing state by adsorbing a dimer BB in the center. Actually, any interface can disappear by itself in a finite amount of time, so there is no infinite dynamic barrier between absorbing states. Therefore the evolution of the interfaces resembles the asymmetric case in Fig. 4.

Absorbing states for $s = 0$ no longer possess the clear-cut global symmetry which drives the system into the DI class. So we expect the system falls into the DP class like the other IMA models without an extra symmetry. We run dynamic Monte Carlo simulations starting with a lattice occupied by monomers at alternating sites except at the central vacant site, $(\cdots A0A0\underline{0}0A0A\cdots)$, where $\underline{0}$ represents a defect. In Fig. 5, we plot three effective exponents against time; $\delta(t)$, $\eta(t)$, and $z(t)$ [2]. Off criticality, these plots show some curvatures. The values of the dynamic scaling exponents can be extracted by taking the asymptotic values of the effective exponents at criticality. From Fig. 5, we estimate $p_c = 0.105(1)$, $\delta = 0.02(1)$, $\eta = 0.48(5)$, and $z = 1.33(5)$. The values of $\delta + \eta$ and z are in good agreement with those of the DP values [18]. Introduction of the symmetry breaking field h only changes the location of p_c. Stationary Monte Carlo simulations also confirm our results [17].

In summary, we found the first IMA model that does not belong to the DP class, but belong to the DI class. This can be achieved by imposing a global Ising symmetry on the absorbing states, i.e., making the two equivalent group of IMA states that are dynamically separated infinitely far apart. When the symmetry between these groups is broken, one group of absorbing states becomes completely obsolete and the evolution morphology changes from a loop-like to a tree-like structure, which ensures the system in the conventional DP class. We also found that the system goes back to the DP class if the mixture-type absorbing states between the two groups are added. These extra absorbing states connect the two separated groups dynamically and make the loop-forming process of the interfaces irrelvant. The absorbing states in all other previously studied IMA models are dynamically connected in the sense as mentioned above. This may explain why those models belong to the DP class.

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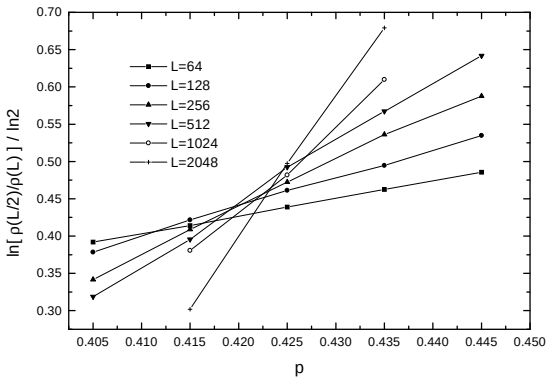

FIG. 1. Plots of $\ln[\rho(L/2)/\rho(L)]/\ln 2$ versus p for the symmetric case.

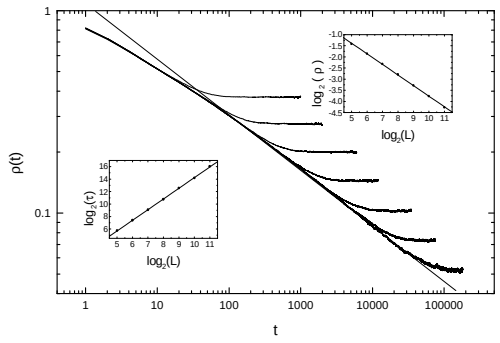

FIG. 2. The time dependence of the kink density at $p_c = 0.425$. The straight line is of slope 0.275 ($= \beta/\nu_\parallel$). Insets show the size dependence of the relaxation time τ and the steady-state kink density ρ at criticality. The solid lines are of slope 1.74 ($= \nu_\parallel/\nu_\perp$) and -0.494 ($= -\beta/\nu_\perp$).

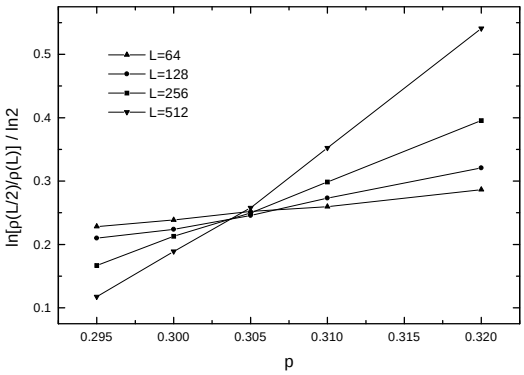

FIG. 3. Plots of $\ln[\rho(L/2)/\rho(L)]/\ln 2$ versus p for the asymmetric case with $h = 0.1$.

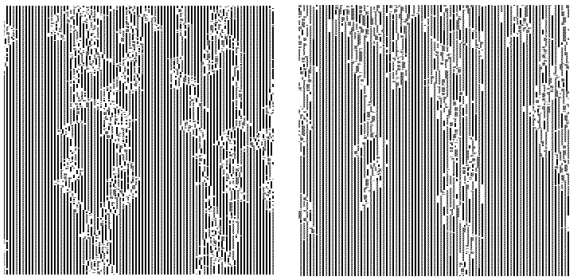

FIG. 4. Evolutions of the critical interfaces for (a) the symmetric case and (b) the asymmetric case. Monomers (A) are represented by black, dimer particles (B) by grey, and vacancies by white pixels.

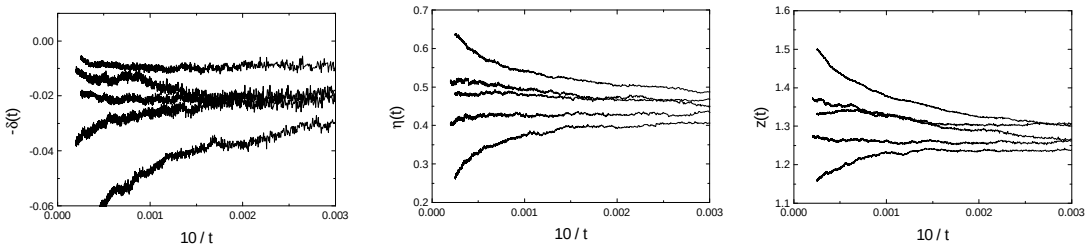

FIG. 5. Plots of the effective exponents against $10/t$ for $s = 0$ and $h = 0$. Five curves from top to botton in each panel correspond to $p = 0.100$, 0.104, 0.105. 0.107, and 0.110.